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30. The method of Claim 29, wherein the first cistron encodes CREB variant Y134F.

31. The method of Claim 22, wherein the first cistron encodes a CREB protein or a variant thereof, and the second cistron encodes a Bcl-2 protein or a Bcl-2 protein having a deletion in the regulatory loop domain.

32. The method of Claim 22, wherein the first cistron encodes a variant E1a protein with a mutation in CR1, and the second cistron encodes an E1b-19K protein, a Bcl-2 protein, or a Bcl-2 protein having a deletion in the regulatory loop domain.

33. The method of Claim 22, wherein the second cistron encodes an apoptosis-protective protein selected from the group consisting of a dominant negative mutant of p53, a protein that interacts with BAX, a protein that interacts with BAK, an inhibitor of apoptosome formation, and a downstream apoptosis inhibitor.

34. The method of Claim 22, wherein the second cistron encodes an adenovirus E1b-19K protein, a Bcl-2 protein, or a Bcl-2 protein having a deletion in the regulatory loop domain.

35. The method of Claim 22, wherein said polypeptide is a single-chain antibody or a heavy or light chain of an antibody or antibody fragment.

36. The method of Claim 22, wherein said polypeptide is a part of a library of polypeptides.

37. A mammalian host cell for recombinant polypeptide expression comprising a first cistron encoding a transactivator protein and a second cistron encoding an apoptosis-protective protein that prevents cell-killing due to expression of the transactivator protein.

38. The host cell of Claim 37, further comprising a third cistron encoding one or more desired polypeptide under the control of a promoter responsive to the transactivator protein.

39. The host cell of Claim 37, wherein the third cistron is associated with a ubiquitous chromatin opening element, an insulator, or a barrier element.

40. The host cell of Claim 37, wherein the transactivator protein is expressed from an efficient heterologous promoter.

MAQAGRTGYDNREIVMKYIHYKLSQRGYEWDVGDVDAAPLG
AAPTPGIFSFQPESNPTPAVHRDMAARTSPLRPIVATTGPT
LSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTA
RGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMS
PLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVELYGPSVRP
LFDFSWLSLKTLLSLALVGACITLGTYLGHK (SEQ ID NO: 1)

FIG. 1

MAQAGRTGYDNREIVMKYIHYKLSQRGYEWDVGDVDAA**AAA**
ASPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTA
RGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMS
PLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVELYGPSVRP
LFDFSWLSLKTLLSLALVGACITLGTYLGHK (SEQ ID NO: 2)

FIG. 2

1 ATGGCTCAAG CTGGGAGAAC AGGGTATGAT AACCGAGAGA TCGTGATGAA

51 GTACATCCAT TATAAGCTGT CACAGAGGGG CTACGAGTGG GATGTGGGAG

101 ATGTGGACGC CGCGGCCGCG GCCGCGAGCC CCGTGCCACC TGTGGTCCAC

151 CTGACCCTCC GCCGGGCTGG GGATGACTTC TCCCGTCGCT ACCGTCGCGA

201 CTTCGCGGAG ATGTCCAGTC AGCTGCACCT GACGCCCTTC ACCGCGAGGG

251 GACGCTTTGC TACGGTGGTG GAGGAACTCT TCAGGGATGG GGTGAACTGG

301 GGGAGGATTG TGGCCTTCTT TGAGTTCGGT GGGGTCATGT GTGTGGAGAG

351 CGTCAACAGG GAGATGTCAC CCCTGGTGGA CAACATCGCC CTGTGGATGA

401 CCGAGTACCT GAACCGGCAT CTGCACACCT GGATCCAGGA TAACGGAGGC

451 TGGGACGCAT TTGTGGAACT GTACGGCCCC AGTGTGAGGC CTCTGTTTGA

501 TTTCTCTTGG CTGTCTCTGA AGACCCTGCT CAGCCTGGCC CTGGTCGGGG

551 CCTGCATCAC TCTGGGTACC TACCTGGGCC ACAAGTGA (SEQ ID NO: 3)

FIG. 3

MRHIICHGGVITEEMAASLLDQLIEEVLADNLPPPSHFE
PPTLHEL**H**DLDVTAPEDPNEEAVSQIFPDSVMLAVQEGI
DLLTFPPAPGSPEPPHLSRQPEQPEQRALGPVSMPNLVP
EVIDLT**G**HEAGFPPSDDEDEEGEEFVLDYVEHPGHGCR
SCHYHRRNTGDPDIMCSLCYMRTCGMFVYSPVSEPEPE
PEPEPEPARPTRRPKMAPAILRRPTSPVSRECNSSTDSCD
SGPSNTPPEIHPVVPLCPIKPVAVRVGGRRQAVECIEDL
LNEPGQPLDLSCKRPRP (SEQ ID NO: 4)

FIG. 4

1 ATGAGACATA TTATCTGCCA CGGAGGTGTT ATTACCGAAG AAATGGCCGC

51 CAGTCTTTTG GACCAGCTGA TCGAAGAGGT ACTGGCTGAT AATCTTCCAC

101 CTCCTAGCCA TTTTGAACCA CCTACCCTTC ACGAACTGCA TGATTTAGAC

151 GTGACGGCCC CCGAAGATCC CAACGAGGAG GCGGTTTCGC AGATTTTTCC

201 CGACTCTGTA ATGTTGGCGG TGCAGGAAGG GATTGACTTA CTCACTTTTC

251 CGCCGGCGCC CGGTTCTCCG GAGCCGCCTC ACCTTTCCCG GCAGCCCGAG

301 CAGCCGGAGC AGAGAGCCTT GGGTCCGGTT TCTATGCCAA ACCTTGTACC

351 GGAGGTGATC GATCTTACCG GCCACGAGGC TGGCTTTCCA CCCAGTGACG

401 ACGAGGATGA AGAGGGTGAG GAGTTTGTGT TAGATTATGT GGAGCACCCC

451 GGGCACGGTT GCAGGTCTTG TCATTATCAC CGGAGGAATA CGGGGGACCC

501 AGATATTATG TGTTCGCTTT GCTATATGAG GACCTGTGGC ATGTTTGTCT

551 ACAGTAAGTG AAAATTATGG GCAGTGGGTG ATAGAGTGGT GGGTTTGGTG

601 TGGTAATTTT TTTTTTAATT TTTACAGTTT TGTGGTTTAA AGAATTTTGT

651 ATTGTGATTT TTTTAAAAGG TCCTGTGTCT GAACCTGAGC CTGAGCCCGA

701 GCCAGAACCG GAGCCTGCAA GACCTACCCG CCGTCCTAAA ATGGCGCCTG

751 CTATCCTGAG ACGCCCGACA TCACCTGTGT CTAGAGAATG CAATAGTAGT

801 ACGGATAGCT GTGACTCCGG TCCTTCTAAC ACACCTCCTG AGATACACCC

851 GGTGGTCCCG CTGTGCCCCA TTAAACCAGT TGCCGTGAGA GTTGGTGGGC

901 GTCGCCAGGC TGTGGAATGT ATCGAGGACT TGCTTAACGA GCCTGGGCAA

951 CCTTTGGACT TGAGCTGTAA ACGCCCCAGG CCATAA (SEQ ID NO: 5)

FIG. 5

1 GAATTCGCCG CCACCATGGA GGCTTGGGAG TGTTTGGAAG ATTTTTCTGC

51 TGTGCGTAAC TTGCTGGAAC AGAGCTCTAA CAGTACCTCT TGGTTTTGGA

101 GGTTTCTGTG GGGCTCATCC CAGGCAAAGT TAGTCTGCAG AATTAAGGAG

151 GATTACAAGT GGGAATTTGA AGAGCTTTTG AAATCCTGTG GTGAGCTGTT

201 TGATTCTTTG AATCTGGGTC ACCAGGCGCT TTTCCAAGAG AAGGTCATCA

251 AGACTTTGGA TTTTTCCACA CCGGGGCGCG CTGCGGCTGC TGTTGCTTTT

301 TTGAGTTTTA TAAAGGATAA ATGGAGCGAA GAAACCCATC TGAGCGGGGG

351 GTACCTGCTG GATTTTCTGG CCATGCATCT GTGGAGAGCG GTTGTGAGAC

401 ACAAGAATCG CCTGCTACTG TTGTCTTCCG TCCGCCCGGC GATAATACCG

451 ACGGAGGAGC AGCAGCAGCA GCAGGAGGAA GCCAGGCGGC GGCGGCAGGA

501 GCAGAGCCCA TGGAACCCGA GAGCCGGCCT GGACCCTCGG GAATGAATGT

551 TGGTCGAC (SEQ ID NO: 15)

FIG. 6

```
    SalI
  1 GTCGACGCCG CCACCATGCC GCCCAAAACC CCCCGAAAAA CGGCCGCCAC
                         M  P   P  K  T   P  R  K  T   A  A  T

 51 CGCCGCCGCT GCCGCCGCGG AACCCCCGGC ACCGCCGCCG CCGCCCCCTC
     A  A  A   A  A  A  E   P  P  A   P  P  P   P  P  P  P

101 CTGAGGAGGA CCCAGAGCAG GACAGCGGCC CGGAGGACCT GCCTCTCGTC
      E  E  D   P  E  Q   D  S  G  P   E  D  L   P  L  V

151 AGGCTTGAGT TTGAAGAAAC AGAAGAACCT GATTTTACTG CATTATGTCA
    R  L  E  F   E  E  T   E  E  P   D  F  T  A   L  C  Q

201 GAAATTAAAG ATACCAGATC ATGTCAGAGA GAGAGCTTGG TTAACTTGGG
     K  L  K   I  P  D  H   V  R  E   R  A  W   L  T  W  E

251 AGAAAGTTTC ATCTGTGGAT GGAGTATTGG GAGGTTATAT TCAAAAGAAA
      K  V  S   S  V  D   G  V  L  G   G  Y  I   Q  K  K

301 AAGGAACTGT GGGGAATCTG TATCTTTATT GCACGAGTTG ACCTAGATGA
    K  E  L  W   G  I  C   I  F  I   A  R  V  D   L  D  E

351 GATGTCGTTC ACTTTACTGA GCTACAGAAA AACATACGAA ATCAGTGTCC
     M  S  F   T  L  L  S   Y  R  K   T  Y  E   I  S  V  H

401 ATAAATTCTT TAACTTACTA AAAGAAATTG ATACCAGTAC CAAAGTTGAT
      K  F  F   N  L  L   K  E  I  D   T  S  T   K  V  D

451 AATGCTATGT CAAGACTGTT GAAGAAGTAT GATGTATTGT TTGCACTCTT
    N  A  M  S   R  L  L   K  K  Y   D  V  L  F   A  L  F

501 CAGCAAATTG GAAAGGACAT GTGAACTTAT ATATTTGACA CAACCCAGCA
     S  K  L   E  R  T  C   E  L  I   Y  L  T   Q  P  S  S

551 GTTCGATATC TACTGAAATA AATTCTGCAT TGGTGCTAAA AGTTTCTTGG
      S  I  S   T  E  I   N  S  A  L   V  L  K   V  S  W

601 ATCACATTTT TATTAGCTAA AGGGGAAGTA TTACAAATGG AAGATGATCT
    I  T  F  L   L  A  K   G  E  V   L  Q  M  E   D  D  L

651 GGTGATTTCA TTTCAGTTAA TGCTATGTGT CCTTGACTAT TTTATTAAAC
     V  I  S   F  Q  L  M   L  C  V   L  D  Y   F  I  K  L
```

FIG. 7A

```
 701 TCTCACCTCC CATGTTGCTC AAAGAACCAT ATAAAACAGC TGTTATACCC
        S  P  P   M  L  L   K  E  P  Y   K  T  A   V  I  P

 751 ATTAATGGTT CACCTCGAAC ACCCAGGCGA GGTCAGAACA GGAGTGCACG
     I  N  G  S   P  R  T   P  R  R   G  Q  N  R   S  A  R

 801 GATAGCAAAA CAACTAGAAA ATGATACAAG AATTATTGAA GTTCTCTGTA
       I  A  K   Q  L  E  N   D  T  R   I  I  E   V  L  C  K

 851 AAGAACATGA ATGTAATATA GATGAGGTGA AAAATGTTTA TTTCAAAAAT
        E  H  E   C  N  I   D  E  V  K   N  V  Y   F  K  N

                         EcoRI
 901 TTTATACCTT TTATGAATTC TCTTGGACTT GTAACATCTA ATGGACTTCC
     F  I  P  F   M  N  S   L  G  L   V  T  S  N   G  L  P

 951 AGAGGTTGAA AATCTTTCTA AACGATACGA AGAAATTTAT CTTAAAAATA
       E  V  E   N  L  S  K   R  Y  E   E  I  Y   L  K  N  K

1001 AAGATCTAGA TCGAAGATTA TTTTTGGATC ATGATAAAAC TCTTCAGACT
        D  L  D   R  R  L   F  L  D  H   D  K  T   L  Q  T

1051 GATTCTATAG ACAGTTTTGA AACACAGAGA ACACCACGAA AAAGTAACCT
     D  S  I  D   S  F  E   T  Q  R   T  P  R  K   S  N  L

1101 TGATGAAGAG GTGAATATAA TTCCTCCACA CACTCCAGTT AGGACTGTTA
       D  E  E   V  N  I  I   P  P  H   T  P  V   R  T  V  M

1151 TGAACACTAT CCAACAATTA ATGATGATTT TAAATTCTGC AAGTGATCAA
        N  T  I   Q  Q  L   M  M  I  L   N  S  A   S  D  Q

1201 CCTTCAGAAA ATCTGATTTC CTATTTTAAC AACTGCACAG TGAATCCAAA
     P  S  E  N   L  I  S   Y  F  N   N  C  T  V   N  P  K

1251 AGAAAGTATA CTGAAAAGAG TGAAGGATAT AGGATACATC TTTAAAGAGA
       E  S  I   L  K  R  V   K  D  I   G  Y  I   F  K  E  K

1301 AATTTGCTAA AGCTGTGGGA CAGGGTTGTG TCGAAATTGG ATCACAGCGA
        F  A  K   A  V  G   Q  G  C  V   E  I  G   S  Q  R

1351 TACAAACTTG GAGTTCGCTT GTATTACCGA GTAATGGAAT CCATGCTTAA
     Y  K  L  G   V  R  L   Y  Y  R   V  M  E  S   M  L  K
```

FIG. 7B

```
1401 ATCAGAAGAA GAACGATTAT CCATTCAAAA TTTTAGCAAA CTTCTGAATG
       S  E  E   E  R  L  S   I  Q  N   F  S  K   L  L  N  D

1451 ACAACATTTT TCATATGTCT TTATTGGCGT GCGCTCTTGA GGTTGTAATG
        N  I  F   H  M  S   L  L  A  C   A  L  E   V  V  M

1501 GCCACATATA GCAGAAGTAC ATCTCAGAAT CTTGATTCTG GAACAGATTT
     A  T  Y  S   R  S  T   S  Q  N   L  D  S  G   T  D  L

1551 GTCTTTCCCA TGGATTCTGA ATGTGCTTAA TTTAAAAGCC TTTGATTTTT
       S  F  P   W  I  L  N   V  L  N   L  K  A   F  D  F  Y

1601 ACAAAGTGAT CGAAAGTTTT ATCAAAGCAG AAGGCAACTT GACAAGAGAA
        K  V  I   E  S  F   I  K  A  E   G  N  L   T  R  E

1651 ATGATAAAAC ATTTAGAACG ATGTGAACAT CGAATCATGG AATCCCTTGC
     M  I  K  H   L  E  R   C  E  H   R  I  M  E   S  L  A

1701 ATGGCTCTCA GATTCACCTT TATTTGATCT TATTAAACAA TCAAAGGACC
       W  L  S   D  S  P  L   F  D  L   I  K  Q   S  K  D  R

1751 GAGAAGGACC AACTGATCAC CTTGAATCTG CTTGTCCTCT TAATCTTCCT
        E  G  P   T  D  H   L  E  S  A   C  P  L   N  L  P

1801 CTCCAGAATA ATCACACTGC AGCAGATATG TATCTTTCTC CTGTAAGATC
     L  Q  N  N   H  T  A   A  D  M   Y  L  S  P   V  R  S

1851 TCCAAAGAAA AAAGGTTCAA CTACGCGTGT AAATTCTACT GCAAATGCAG
       P  K  K   K  G  S  T   T  R  V   N  S  T   A  N  A  E

1901 AGACACAAGC AACCTCAGCC TTCCAGACCC AGAAGCCATT GAAATCTACC
        T  Q  A   T  S  A   F  Q  T  Q   K  P  L   K  S  T

1951 TCTCTTTCAC TGTTTTATAA AAAAGTGTAT CGGCTAGCCT ATCTCCGGCT
     S  L  S  L   F  Y  K   K  V  Y   R  L  A  Y   L  R  L

2001 AAATACACTT TGTGAACGCC TTCTGTCTGA GCACCCAGAA TTAGAACATA
       N  T  L   C  E  R  L   L  S  E   H  P  E   L  E  H  I

2051 TCATCTGGAC CCTTTTCCAG CACACCCTGC AGAATGAGTA TGAACTCATG
        I  W  T   L  F  Q   H  T  L  Q   N  E  Y   E  L  M
```

FIG. 7C

```
2101 AGAGACAGGC ATTTGGACCA AATTATGATG TGTTCCATGT ATGGCATATG
     R  D  R  H   L  D  Q   I  M  M   C  S  M  Y   G  I  C

2151 CAAAGTGAAG AATATAGACC TTAAATTCAA AATCATTGTA ACAGCATACA
      K  V  K   N  I  D  L   K  F  K   I  I  V   T  A  Y  K

2201 AGGATCTTCC TCATGCTGTT CAGGAGACAT TCAAACGTGT TTTGATCAAA
       D  L  P   H  A  V   Q  E  T  F   K  R  V   L  I  K

2251 GAAGAGGAGT ATGATTCTAT TATAGTATTC TATAACTCGG TCTTCATGCA
     E  E  E  Y   D  S  I   I  V  F   Y  N  S  V   F  M  Q

2301 GAGACTGAAA ACAAATATTT TGCAGTATGC TTCCACCAGG CCCCCTACCT
      R  L  K   T  N  I  L   Q  Y  A   S  T  R   P  P  T  L

2351 TGTCACCAAT ACCTCACATT CCTCGAAGCC CTTACAAGTT TCCTAGTTCA
       S  P  I   P  H  I   P  R  S  P   Y  K  F   P  S  S

2401 CCCTTACGGA TTCCTGGAGG GAACATCTAT ATTTCACCCC TGAAGAGTCC
     P  L  R  I   P  G  G   N  I  Y   I  S  P  L   K  S  P

2451 ATATAAAATT TCAGAAGGTC TGCCAACACC AACAAAAATG ACTCCAAGAT
      Y  K  I   S  E  G  L   P  T  P   T  K  M   T  P  R  S

2501 CAAGAATCTT AGTATCAATT GGTGAATCAT TCGGGACTTC TGAGAAGTTC
       R  I  L   V  S  I   G  E  S  F   G  T  S   E  K  F

2551 CAGAAAATAA ATCAGATGGT ATGTAACAGC GACCGTGTGC TCAAAAGAAG
     Q  K  I  N   Q  M  V   C  N  S   D  R  V  L   K  R  S

2601 TGCTGAAGGA AGCAACCCTC CTAAACCACT GAAAAAACTA CGCTTTGATA
      A  E  G   S  N  P  P   K  P  L   K  K  L   R  F  D  I

2651 TTGAAGGATC AGATGAAGCA GATGGAAGTA AACATCTCCC AGGAGAGTCC
       E  G  S   D  E  A   D  G  S  K   H  L  P   G  E  S

2701 AAATTTCAGC AGAAACTGGC AGAAATGACT TCTACTCGAA CACGAATGCA
     K  F  Q  Q   K  L  A   E  M  T   S  T  R  T   R  M  Q

2751 AAAGCAGAAA ATGAATGATA GCATGGATAC CTCAAACAAG GAAGAGAAAT
      K  Q  K   M  N  D  S   M  D  T   S  N  K   E  E  K  *

                             NotI
2801 GAGGATCTCA GGACCGGCGG CCGC
```

FIG. 7D

```
    EcoRI
  1 GAATTCGCCG CCACCATGAC CATGGACTCT GGAGCAGACA ACCAGCAGAG
                   M  T    M  D  S   G  A  D  N   Q  Q  S

 51 TGGAGATGCA GCTGTAACAG AAGCTGAAAA CCAACAAATG ACAGTTCAAG
     G  D  A   A  V  T  E   A  E  N   Q  Q  M   T  V  Q  A

101 CCCAGCCACA GATTGCCACA TTAGCCCAGG TATCTATGCC AGCAGCTCAT
      Q  P  Q   I  A  T   L  A  Q  V   S  M  P   A  A  H

151 GCAACATCAT CTGCTCCCAC CGTAACTCTA GTACAGCTGC CCAATGGGCA
    A  T  S  S   A  P  T   V  T  L   V  Q  L  P   N  G  Q

201 GACAGTTCAA GTCCATGGAG TCATTCAGGC GGCCCAGCCA TCAGTTATTC
     T  V  Q   V  H  G  V   I  Q  A   A  Q  P   S  V  I  Q

251 AGTCTCCACA AGTCCAAACA GTTCAGATTT CAACTATTGC AGAAAGTGAA
      S  P  Q   V  Q  T   V  Q  I  S   T  I  A   E  S  E

301 GATTCACAGG AGTCAGTGGA TAGTGTAACT GATTCCCAAA AGCGAAGGGA
    D  S  Q  E   S  V  D   S  V  T   D  S  Q  K   R  R  E

351 AATTCTTTCA AGGAGGCCTT CCTTCAGGAA AATTTTGAAT GACTTATCTT
     I  L  S   R  R  P  S   F  R  K   I  L  N   D  L  S  S

401 CTGATGCACC AGGAGTGCCA AGGATTGAAG AAGAGAAGTC TGAAGAGGAG
      D  A  P   G  V  P   R  I  E  E   E  K  S   E  E  E

451 GCTTCAGCAC CTGCCATCAC CGCTGTAGCG GTGCCAACGC CAATTTACCG
    A  S  A  P   A  I  T   A  V  A   V  P  T  P   I  Y  R

501 GACTAGCAGT GGACAGTATA TTACCATTAC CCAGAGAGGA GCAATACAGC
     T  S  S   G  Q  Y  I   T  I  T   Q  R  G   A  I  Q  L

551 TGGCTAGCAA TGGTACCGAT GGGGTACAGG GCCTGCAAAC ATTAACCATG
      A  S  N   G  T  D   G  V  Q  G   L  Q  T   L  T  M

601 GCCAATGCAG CAGCCACTCA GCCCGGTACT ACCATTCTAC AGTATGCACA
    A  N  A  A   A  T  Q   P  G  T   T  I  L  Q   Y  A  Q

651 GACCACTGAT GGACAGCAGA TCTTAGTGCC CAGCAACCAA GTTGTTGTTC
     T  T  D   G  Q  Q  I   L  V  P   S  N  Q   V  V  V  Q
```

FIG. 8A

```
701 AAGCTGCCTC TGGAGACGTA CAAACATACC AGATTCGCAC AGCACCCACT
      A  A  S   G  D  V   Q  T  Y  Q   I  R  T   A  P  T

751 AGCACTATTG CCCCTGGAGT TGTTATGGCA TCCTCCCCAG CACTTCCTAC
    S  T  I  A   P  G  V   V  M  A   S  S  P  A   L  P  T

801 ACAGCCTGCT GAAGAAGCAG CACGAAAGAG AGAGGTCCGT CTAATGAAGA
     Q  P  A   E  E  A  A   R  K  R   E  V  R   L  M  K  N

851 ACAGGGAAGC AGCTCGTGAG TGTCGTAGAA AGAAGAAAGA ATATGTGAAA
      R  E  A   A  R  E   C  R  R  K   K  K  E   Y  V  K

901 TGTTTAGAAA ACAGAGTGGC AGTGCTTGAA AATCAAAACA AGACATTGAT
    C  L  E  N   R  V  A   V  L  E   N  Q  N  K   T  L  I

951 TGAGGAGCTA AAAGCACTTA AGGACCTTTA CTGCCACAAA TCAGATTAAT
     E  E  L   K  A  L  K   D  L  Y   C  H  K   S  D  *

        SalI
1001 TTGGGTCGAC
```

FIG. 8B

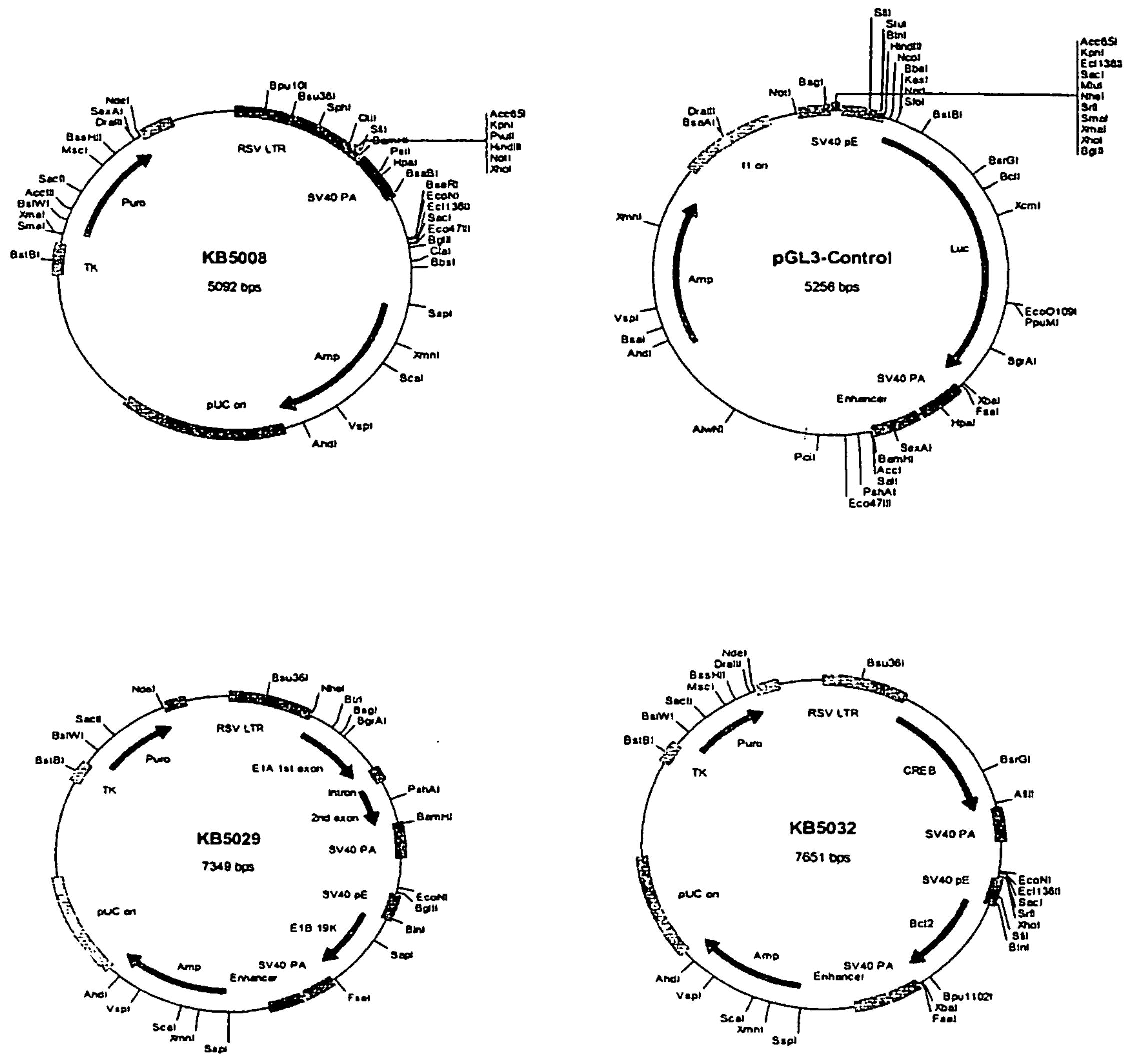

Figure 9. Maps of KB5008, pGL3-Control, KB5029, and KB5032.

KB5008 carries a RSVLTR promoter and was used to clone E1a and CREB. pGL3-Control carries a SV40 promoter and was used to clone E1b-19K and Bcl2. KB5029 carries the double expression cassettes for E1a and E1b-19K. KB5032 carries the double expression cassettes for CREB and Bcl2.

```
1    aagcttgccg ccaccatgag acatattatc tgccacggag gtgttattac
     HindIII            M  R  H  I  I  C  H  G  G  V  I
51   cgaagaaatg gccgccagtc ttttggacca gctgatcgaa gaggtactgg
     T  E  E  M  A  A  S  L  L  D  Q  L  I  E  E  V  L
101  ctgataatct tccacctcct agccattttg aaccacctac ccttcacgaa
     A  D  N  L  P  P  P  S  H  F  E  P  P  T  L  H  E
151  ctgtatgatt tagacgtgac ggcccccgaa gatcccaacg aggaggcggt
     L  Y  D  L  D  V  T  A  P  E  D  P  N  E  E  A
201  ttcgcagatt tttcccgact ctgtaatgtt ggcggtgcag gaagggattg
     V  S  Q  I  F  P  D  S  V  M  L  A  V  Q  E  G  I
251  acttactcac ttttccgccg gcgcccggtt ctccggagcc gcctcacctt
     D  L  L  T  F  P  P  A  P  G  S  P  E  P  P  H  L
301  tcccggcagc ccgagcagcc ggagcagaga gccttgggtc cggtttctat
     S  R  Q  P  E  Q  P  E  Q  R  A  L  G  P  V  S
351  gccaaacctt gtaccggagg tgatcgatct tacctgccac gaggctggct
     M  P  N  L  V  P  E  V  I  D  L  T  C  H  E  A  G
401  ttccacccag tgacgacgag gatgaagagg gtgaggagtt tgtgttagat
     F  P  P  S  D  D  E  D  E  E  G  E  E  F  V  L  D
451  tatgtggagc accccgggca cggttgcagg tcttgtcatt atcaccggag
     Y  V  E  H  P  G  H  G  C  R  S  C  H  Y  H  R
501  gaatacgggg gacccagata ttatgtgttc gctttgctat atgaggacct
     R  N  T  G  D  P  D  I  M  C  S  L  C  Y  M  R  T
551  gtggcatgtt tgtctacagt cctgtgtctg aacctgagcc tgagcccgag
     C  G  M  F  V  Y  S  P  V  S  E  P  E  P  E  P  E
601  ccagaaccgg agcctgcaag acctacccgc cgtcctaaaa tggcgcctgc
     P  E  P  E  P  A  R  P  T  R  R  P  K  M  A  P
651  tatcctgaga cgcccgacat cacctgtgtc tagagaatgc aatagtagta
     A  I  L  R  R  P  T  S  P  V  S  R  E  C  N  S  S
701  cggatagctg tgactccggt ccttctaaca cacctcctga gatacacccg
     T  D  S  C  D  S  G  P  S  N  T  P  P  E  I  H  P
751  gtggtcccgc tgtgccccat taaaccagtt gccgtgagag ttggtgggcg
     V  V  P  L  C  P  I  K  P  V  A  V  R  V  G  G
801  tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac
     R  R  Q  A  V  E  C  I  E  D  L  L  N  E  P  G  Q
851  ctttggactt gagctgtaaa cgccccaggc cataactcga g
     P  L  D  L  S  C  K  R  P  R  P  -  XhoI
```

Figure 10. Nucleotide coding sequence of E1a cDNA (SEQ ID NO: 40). Cloning sites HindIII and XhoI, and two amino acid residue positions Y47 and C124 are underscored.

```
1    aagcttgccg ccaccatgag acatattatc tgccacggag gtgttattac
       HindIII         M    R  H  I  I   C  H  G   G  V  I

51   cgaagaaatg gccgccagtc ttttggacca gctgatcgaa gaggtactgg
     T  E  E  M   A  A  S   L  L  D   Q  L  I  E   E  V  L

101  ctgataatct tccacctcct agccattttg aaccacctac ccttcacgaa
      A  D  N   L  P  P  P   S  H  F   E  P  P   T  L  H  E

151  ctgcatgatt tagacgtgac ggcccccgaa gatcccaacg aggaggcggt
      L  H  D   L  D  V   T  A  P  E   D  P  N   E  E  A

201  ttcgcagatt tttcccgact ctgtaatgtt ggcggtgcag gaagggattg
     V  S  Q  I   F  P  D   S  V  M   L  A  V  Q   E  G  I

251  acttactcac ttttccgccg gcgcccggtt ctccggagcc gcctcacctt
      D  L  L   T  F  P  P   A  P  G   S  P  E   P  P  H  L

301  tcccggcagc ccgagcagcc ggagcagaga gccttgggtc cggtttctat
      S  R  Q   P  E  Q   P  E  Q  R   A  L  G   P  V  S

351  gccaaacctt gtaccggagg tgatcgatct tacctgccac gaggctggct
     M  P  N  L   V  P  E   V  I  D   L  T  C  H   E  A  G

401  ttccacccag tgacgacgag gatgaagagg gtgaggagtt tgtgttagat
      F  P  P   S  D  D  E   D  E  E   G  E  E   F  V  L  D

451  tatgtggagc accccgggca cggttgcagg tcttgtcatt atcaccggag
      Y  V  E   H  P  G   H  G  C  R   S  C  H   Y  H  R

501  gaatacgggg gacccagata ttatgtgttc gctttgctat atgaggacct
     R  N  T  G   D  P  D   I  M  C   S  L  C  Y   M  R  T

551  gtggcatgtt tgtctacagt cctgtgtctg aacctgagcc tgagcccgag
      C  G  M   F  V  Y  S   P  V  S   E  P  E   P  E  P  E

601  ccagaaccgg agcctgcaag acctacccgc cgtcctaaaa tggcgcctgc
      P  E  P   E  P  A   R  P  T  R   R  P  K   M  A  P

651  tatcctgaga cgcccgacat cacctgtgtc tagagaatgc aatagtagta
     A  I  L  R   R  P  T   S  P  V   S  R  E  C   N  S  S

701  cggatagctg tgactccggt ccttctaaca cacctcctga gatacacccg
      T  D  S   C  D  S  G   P  S  N   T  P  P   E  I  H  P

751  gtggtcccgc tgtgccccat taaaccagtt gccgtgagag ttggtgggcg
      V  V  P   L  C  P   I  K  P  V   A  V  R   V  G  G

801  tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac
     R  R  Q  A   V  E  C   I  E  D   L  L  N  E   P  G  Q

851  ctttggactt gagctgtaaa cgccccaggc cataactcga g
      P  L  D   L  S  C  K   R  P  R   P  -  XhoI
```

Figure 11. Nucleotide coding sequence of E1a_Y47H (SEQ ID NO: 41). Cloning sites HindIII and XhoI are underscored.

```
1     aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag
      HindIII           M   T  M  E  S   G  A  D   N  Q  Q

51    tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag
      S  G  D  A   A  V  T   E  A  E   N  Q  Q  M   T  A  Q

101   cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat
       A  Q  P   Q  I  A  T   L  A  Q   V  S  M   P  A  A  H

151   gcgacatcat ctgctcccac tgtaacctta gtgcagctgc ccaatgggca
       A  T  S    S  A  P   T  V  T  L   V  Q  L   P  N  G

201   gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc
      Q  T  V  Q   V  H  G   V  I  Q   A  A  Q  P   S  V  I

251   agtctccaca agtccaaaca gttcagtctt cctgtaagga cttaaaaaga
       Q  S  P   Q  V  Q  T   V  Q  S   S  C  K   D  L  K  R

301   cttttctccg gaactcagat ttcaactatt gcagaaagtg aggattcaca
        L  F  S   G  T  Q   I  S  T  I   A  E  S   E  D  S

351   ggaatctgtg gatagtgtaa ctgattccca aaagcgaagg gaaattcttt
      Q  E  S  V   D  S  V   T  D  S   Q  K  R  R   E  I  L

401   caaggaggcc ttcctacagg aaaattttga atgacttatc ttctgatgca
       S  R  R   P  S  Y  R   K  I  L   N  D  L   S  S  D  A

451   ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc
        P  G  V   P  R  I   E  E  E  K   S  E  E   E  T  S

501   ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca
      A  P  A  I   T  T  V   T  V  P   T  P  I  Y   Q  T  S

551   gtgggcagta tattgccatt acccagggag gagctataca gctggctaac
       S  G  Q   Y  I  A  I   T  Q  G   G  A  I   Q  L  A  N

601   aatggtaccg atggggtaca gggccttcag acattaacca tgaccaatgc
        N  G  T   D  G  V   Q  G  L  Q   T  L  T   M  T  N

651   agctgccact cagccgggta ccactattct acagtatgca cagaccactg
      A  A  A  T   Q  P  G   T  T  I   L  Q  Y  A   Q  T  T

701   atggacagca gattctagtg cccagcaacc aagttgttgt tcaagctgcc
       D  G  Q   Q  I  L  V   P  S  N   Q  V  V   V  Q  A  A

751   tctggcgatg tacaaacata ccaaattcgt acagcaccca ctagcaccat
        S  G  D   V  Q  T   Y  Q  I  R   T  A  P   T  S  T

801   cgcccctgga gttgttatgg catcctcccc agcacttcct acgcagcctg
      I  A  P  G   V  V  M   A  S  S   P  A  L  P   T  Q  P

851   ctgaagaagc agcccggaag agagaggttc gtctaatgaa gaacagggaa
       A  E  E   A  A  R  K   R  E  V   R  L  M   K  N  R  E

901   gcagcaagag aatgtcgtag aaagaagaaa gaatatgtga aatgtttaga
       A  A  R   E  C  R   R  K  K  K   E  Y  V   K  C  L

951   gaacagagtg gcagtgcttg aaaaccaaaa caagacattg attgaggagc
      E  N  R  V   A  V  L   E  N  Q   N  K  T  L   I  E  E

1001  taaaagcact taaggacctt tactgccaca aatcagatta aggatcc
       L  K  A   L  K  D  L   Y  C  H   K  S  D   -  BamHI
```

Figure 12. Nucleotide coding sequence of hamster CREB-B cDNA (SEQ ID NO: 42). Cloning sites HindIII and BamHI are underscored.

```
1     aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag
      HindIII            M  T  M  E  S  G  A  D  N  Q  Q
51    tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag
      S  G  D  A  A  V  T  E  A  E  N  Q  Q  M  T  A  Q
101   cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat
      A  Q  P  Q  I  A  T  L  A  Q  V  S  M  P  A  A  H
151   gcgacatcat ctgctcccac tgtaacctta gtgcagctgc ccaatgggca
      A  T  S  S  A  P  T  V  T  L  V  Q  L  P  N  G
201   gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc
      Q  T  V  Q  V  H  G  V  I  Q  A  A  Q  P  S  V  I
251   agtctccaca agtccaaaca gttcagtctt cctgtaagga cttaaaaaga
      Q  S  P  Q  V  Q  T  V  Q  S  S  C  K  D  L  K  R
301   cttttctccg gaactcagat ttcaactatt gcagaaagtg aggattcaca
      L  F  S  G  T  Q  I  S  T  I  A  E  S  E  D  S
351   ggaatctgtg gatagtgtaa ctgattccca aaagcgaagg gaaattcttt
      Q  E  S  V  D  S  V  T  D  S  Q  K  R  R  E  I  L
401   caaggaggcc ttcctccagg aaaattttga atgacttatc ttctgatgca
      S  R  R  P  S  F  R  K  I  L  N  D  L  S  S  D  A
451   ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc
      P  G  V  P  R  I  E  E  E  K  S  E  E  E  T  S
501   ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca
      A  P  A  I  T  T  V  T  V  P  T  P  I  Y  Q  T  S
551   gtgggcagta tattgccatt acccagggag gagctataca gctggctaac
      S  G  Q  Y  I  A  I  T  Q  G  G  A  I  Q  L  A  N
601   aatggtaccg atggggtaca gggccttcag acattaacca tgaccaatgc
      N  G  T  D  G  V  Q  G  L  Q  T  L  T  M  T  N
651   agctgccact cagccgggta ccactattct acagtatgca cagaccactg
      A  A  A  T  Q  P  G  T  T  I  L  Q  Y  A  Q  T  T
701   atggacagca gattctagtg cccagcaacc aagttgttgt tcaagctgcc
      D  G  Q  Q  I  L  V  P  S  N  Q  V  V  V  Q  A  A
751   tctggcgatg tacaaacata ccaaattcgt acagcaccca ctagcaccat
      S  G  D  V  Q  T  Y  Q  I  R  T  A  P  T  S  T
801   cgcccctgga gttgttatgg catcctcccc agcacttcct acgcagcctg
      I  A  P  G  V  V  M  A  S  S  P  A  L  P  T  Q  P
851   ctgaagaagc agcccggaag agagaggttc gtctaatgaa gaacagggaa
      A  E  E  A  A  R  K  R  E  V  R  L  M  K  N  R  E
901   gcagcaagag aatgtcgtag aaagaagaaa gaatatgtga aatgtttaga
      A  A  R  E  C  R  R  K  K  K  E  Y  V  K  C  L
951   gaacagagtg gcagtgcttg aaaaccaaaa caagacattg attgaggagc
      E  N  R  V  A  V  L  E  N  Q  N  K  T  L  I  E  E
1001  taaaagcact taaggacctt tactgccaca aatcagatta aggatcc
      L  K  A  L  K  D  L  Y  C  H  K  S  D  -  BamHI
```

Figure 13. Nucleotide coding sequence of hamster CREB-B Y134F cDNA (SEQ ID NO: 43). Cloning sites HindIII and BamHI are underscored.

```
1    aagcttactg ttggtaaagc cgccaccatg gaggcttggg agtgtttgga
     HindIII                         M   E  A  W   E  C  L

51   agatttttct gctgtgcgta acttgctgga acagagctct aacagtacct
     E  D  F  S   A  V  R   N  L  L   E  Q  S  S   N  S  T

101  cttggttttg gaggtttctg tggggctcat cccaggcaaa gttagtctgc
      S  W  F   W  R  F  L   W  G  S   S  Q  A   K  L  V  C

151  agaattaagg aggattacaa gtgggaattt gaagagcttt tgaaatcctg
       R  I  K   E  D  Y   K  W  E  F   E  E  L   L  K  S

201  tggtgagctg tttgattctt tgaatctggg tcaccaggcg cttttccaag
     C  G  E  L   F  D  S   L  N  L   G  H  Q  A   L  F  Q

251  agaaggtcat caagactttg gatttttcca caccggggcg cgctgcggct
      E  K  V   I  K  T  L   D  F  S   T  P  G   R  A  A  A

301  gctgttgctt ttttgagttt tataaaggat aaatggagcg aagaaaccca
       A  V  A   F  L  S   F  I  K  D   K  W  S   E  E  T

351  tctgagcggg gggtacctgc tggattttct ggccatgcat ctgtggagag
     H  L  S  G   G  Y  L   L  D  F   L  A  M  H   L  W  R

401  cggttgtgag acacaagaat cgcctgctac tgttgtcttc cgtccgcccg
       A  V  V   R  H  K  N   R  L  L   L  L  S   S  V  R  P

451  gcgataatac cgacggagga gcagcagcag cagcaggagg aagccaggcg
       A  I  I   P  T  E   E  Q  Q  Q   Q  Q  E   E  A  R

501  gcggcggcag gagcagagcc catggaaccc gagagccggc ctggaccctc
     R  R  R  Q   E  Q  S   P  W  N   P  R  A  G   L  D  P

551  gggaatgatc taga
       R  E  -  XbaI
```

Figure 14. Nucleotide coding sequence of E1b-19K (SEQ ID NO: 44). **Cloning sites HindIII and XbaI are underscored.**

```
     NcoI
  1  ccatggctca agctgggaga acagggtatg ataaccgaga gatcgtgatg
           M  A   Q  A  G  R   T  G  Y   D  N  R   E  I  V  M

 51  aagtacatcc attataagct gtcacagagg ggctacgagt gggatgtggg
       K  Y  I   H  Y  K   L  S  Q  R   G  Y  E   W  D  V

101  agatgtggac gccgcggccg cggccgcgag ccccgtgcca cctgtggtcc
     G  D  V  D   A  A  A   A  A  A   S  P  V  P   P  V  V

151  acctgaccct ccgccgggct ggggatgact tctcccgtcg ctaccgtcgc
       H  L  T   L  R  R  A   G  D  D   F  S  R   R  Y  R  R

201  gacttcgcgg agatgtccag tcagctgcac ctgacgccct tcaccgcgag
       D  F  A   E  M  S   S  Q  L  H   L  T  P   F  T  A

251  gggacgcttt gctacggtgg tggaggaact cttcagggat ggggtgaact
     R  G  R  F   A  T  V   V  E  E   L  F  R  D   G  V  N

301  gggggaggat tgtggccttc tttgagttcg gtggggtcat gtgtgtggag
       W  G  R   I  V  A  F   F  E  F   G  G  V   M  C  V  E

351  agcgtcaaca gggagatgtc acccctggtg gacaacatcg ccctgtggat
       S  V  N   R  E  M   S  P  L  V   D  N  I   A  L  W

401  gaccgagtac ctgaaccggc atctgcacac ctggatccag gataacggag
     M  T  E  Y   L  N  R   H  L  H   T  W  I  Q   D  N  G

451  gctgggacgc atttgtggaa ctgtacggcc ccagtgtgag gcctctgttt
       G  W  D   A  F  V  E   L  Y  G   P  S  V   R  P  L  F

501  gatttctctt ggctgtctct gaagaccctg ctcagcctgg ccctggtcgg
       D  F  S   W  L  S   L  K  T  L   L  S  L   A  L  V

551  ggcctgcatc actctgggta cctacctggg ccacaagtga tctaga
     G  A  C  I   T  L  G   T  Y  L   G  H  K  -   XbaI
```

Figure 15. Nucleotide coding sequence of hamster Bcl2 deletion mutant (SEQ ID NO: 45). Cloning sites NcoI and XbaI are underscored.

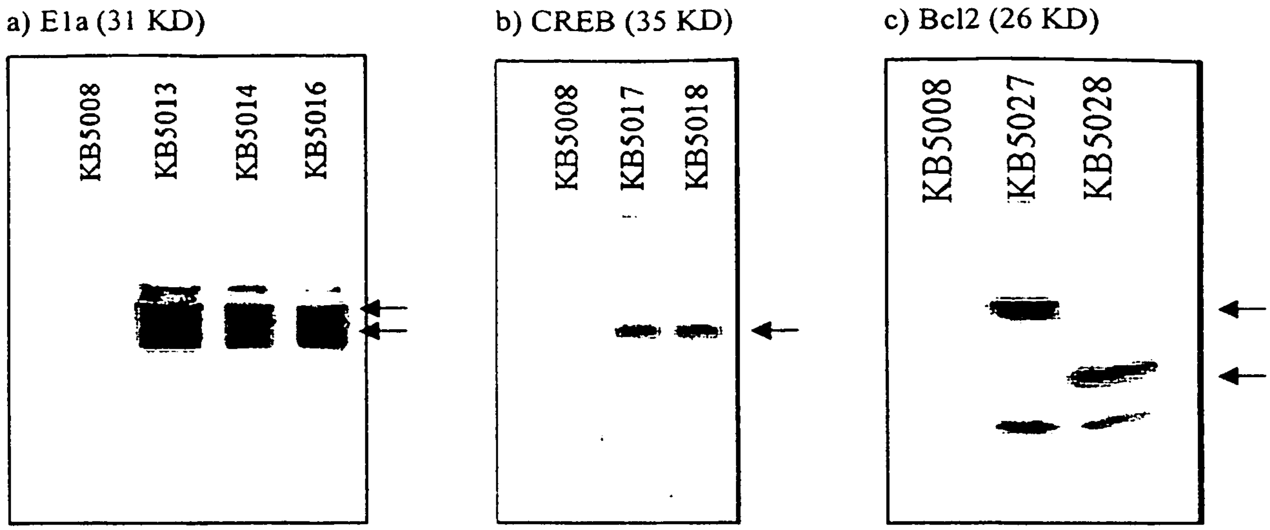

Figure 16. Western blots of E1a, CREB and Bcl2.

In a), b), and c), 1×10^5 CHO-K1 cells were transfected with 0.4 μg of indicated plasmid DNA. Cell lysates were collected after 48 hours and probed with appropriate antibodies. KB5008 transfected cells were used as negative controles.

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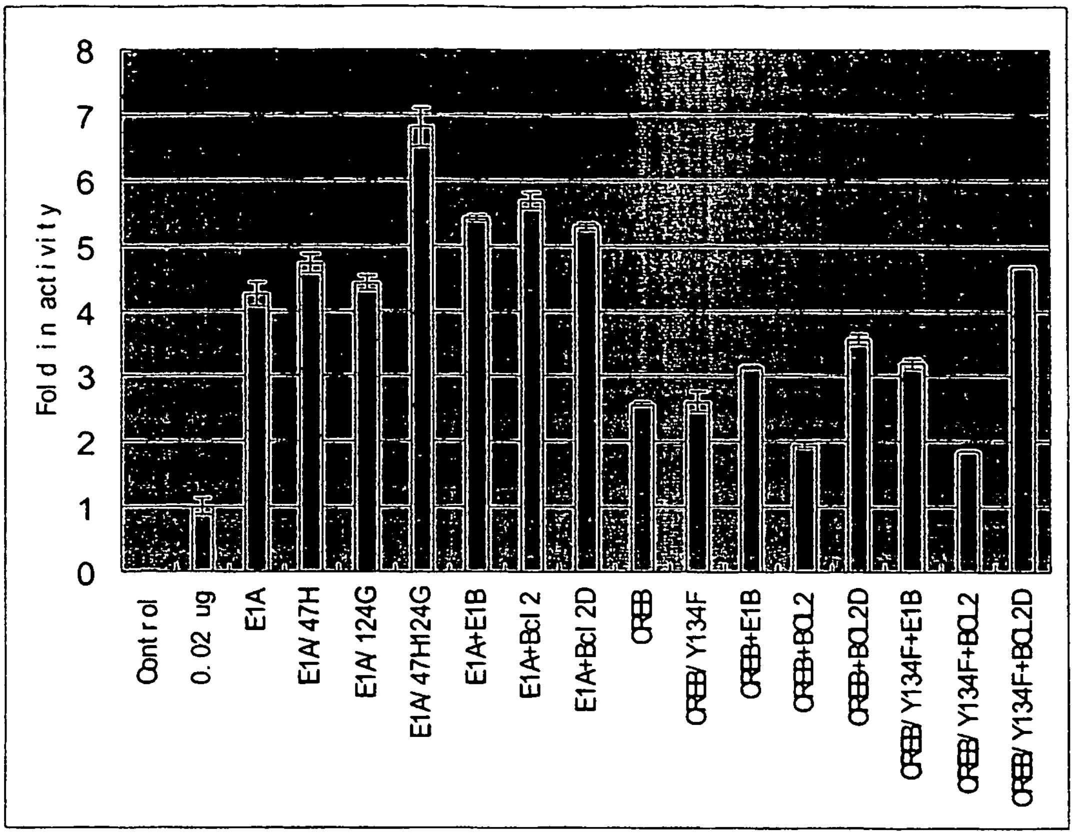

Figure 17. E1a and CREB enhanced CMV promoter in CHO-K1 cells.
1×10^5 cells were transfected with 0.02 μg of SEAP reporter construct KB5019 and 0.2 μg of E1a or CREB expressing constructs. Total DNA was added up to 0.4 μg/well by control plasmid KB5008, E1b-19K or Bcl2 expressing plasmids. SEAP activities from culture media were assay 48 hours after transfection. The control was mock transfected CHO-K1 cells.

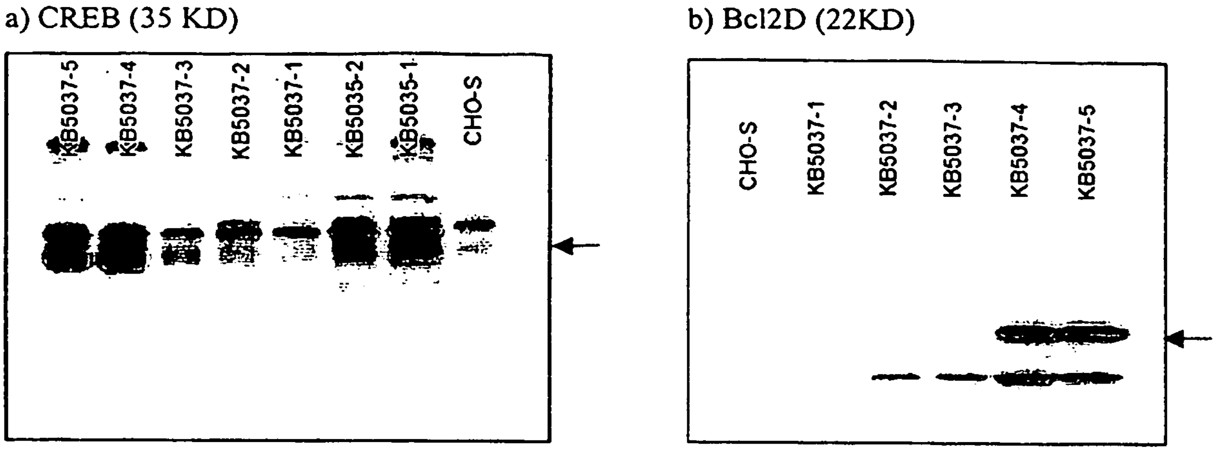

Figure 18. Western blots showing overexpression of hamster CREB-B Y134F and hamster ΔBcl-2 in stable transfectant CHO-S cell lines.